

unaltered

; Sequence 3, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
; APPLICANT: Dior I. Baruch
; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidig
; APPLICANT: Jurg Gysin
; APPLICANT: Bruno Pouvelle
; APPLICANT: Nobutaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; TITLE OF INVENTION: (PFEMP1) THAT MEDIATES ADHESION TO CHONDRITIN SULFATE A
; FILE REFERENCE: NIH176_001C1
; CURRENT APPLICATION NUMBER: US/10/087.013
; CURRENT FILING DATE: 2002-02-21
; PRIORITY APPLICATION NUMBER: PCT/US00/24195
; PRIORITY FILING DATE: 2000-09-01
; PRIORITY APPLICATION NUMBER: 60/152,023
; PRIORITY FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3 ;
; LENGTH: 32 ;
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-087-013-3
; KELKEKGKIPPEGKRMQFTFGYRDILFG1
;
; Sequence 4, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
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; PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
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; PRIORITY FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4 ;
; LENGTH: 10 ;
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-087-013-4
; KELKEKGKIPPEGKRMQFTFGYRDILFG1

PEPB = residues 1279 - 1554 of seq ID# 2

pepb.pep
GENERAL INFORMATION:

APPLICANT: Arthur Scherf
APPLICANT: Louis H. Miller
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APPLICANT: Christine Scheidig

APPLICANT: Jurg Gysin
APPLICANT: Bruno Povelle
APPLICANT: Nobutaka Fujii

APPLICANT: Joseph Smith

TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF PLASMODIUM FALCIPARUM ERTHROCYTE MEMBRANE PROTEIN 1

TITLE OF INVENTION: (PFEMP1) THAT MEDIATES ADHESION TO CHONDRITIN SULFATE A

FILE REFERENCE: NIH176_001C1

CURRENT APPLICATION NUMBER: US110/087,013

PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/152,023

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 3542

TYPE: PRT

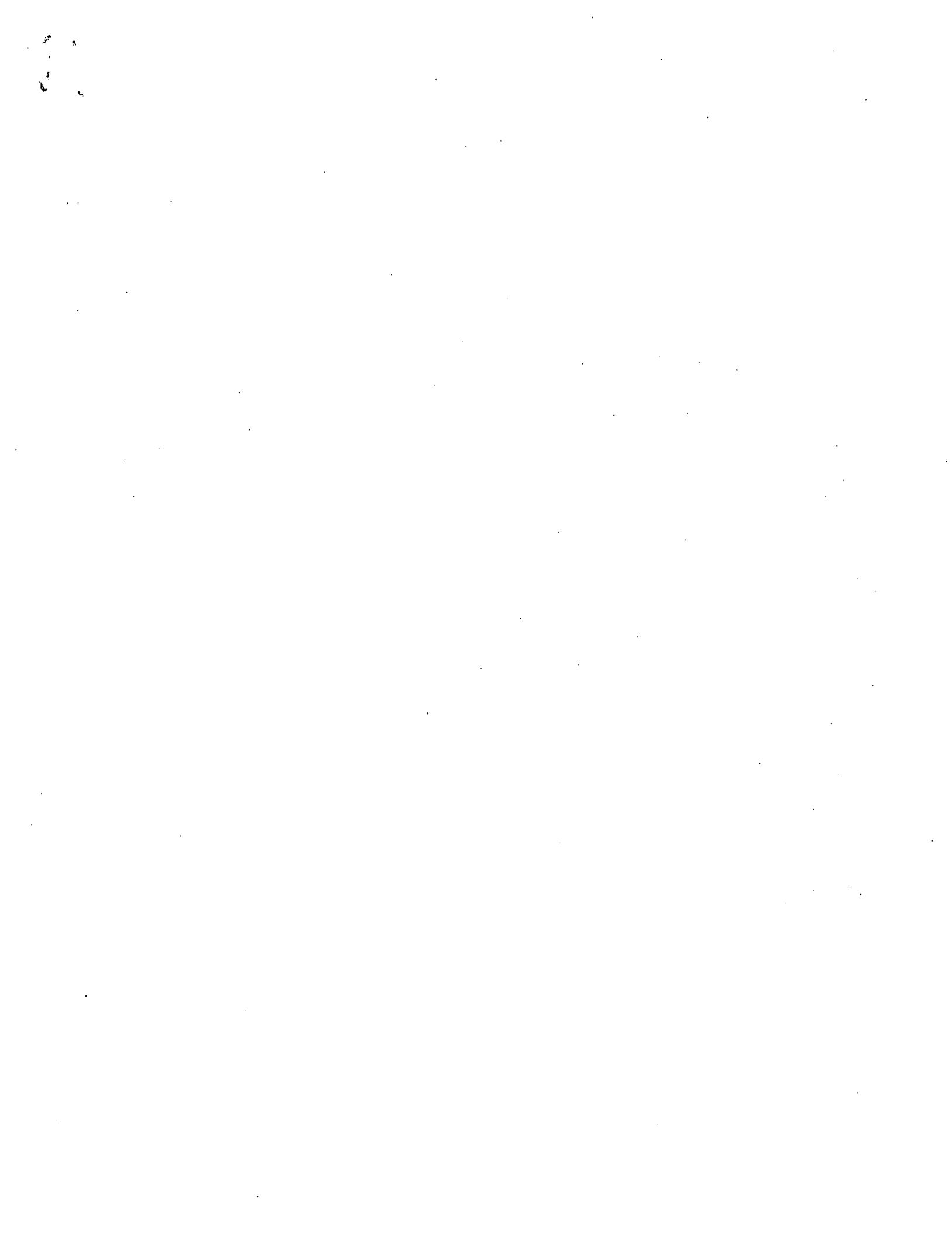
ORGANISM: Plasmodium falciparu

PEPB_PEP

DCHPRKNSNYPDQCGNINLVEPRVCHPPRQLCVHFLANDNEIKLQSQVNLFERAFIKSAAAETPFWYVKKSKOEGNEILDEKLKEGKPPAFRSMEFTFGYDFEGLTDISKHGEGSKIKEQIDSLFKNGDOKSGNGKTRQEWWEHSHEIWEMALCKIGAKRDKDFTENYGNVNVFSDKTILEFAKRQFLRMLTWYDDCYTROKYLKDVOEKCKSNNDQLKCDTECNKCKEDYVKYMKKKKEWIPQDQYYKDERDKRFL

276

residues



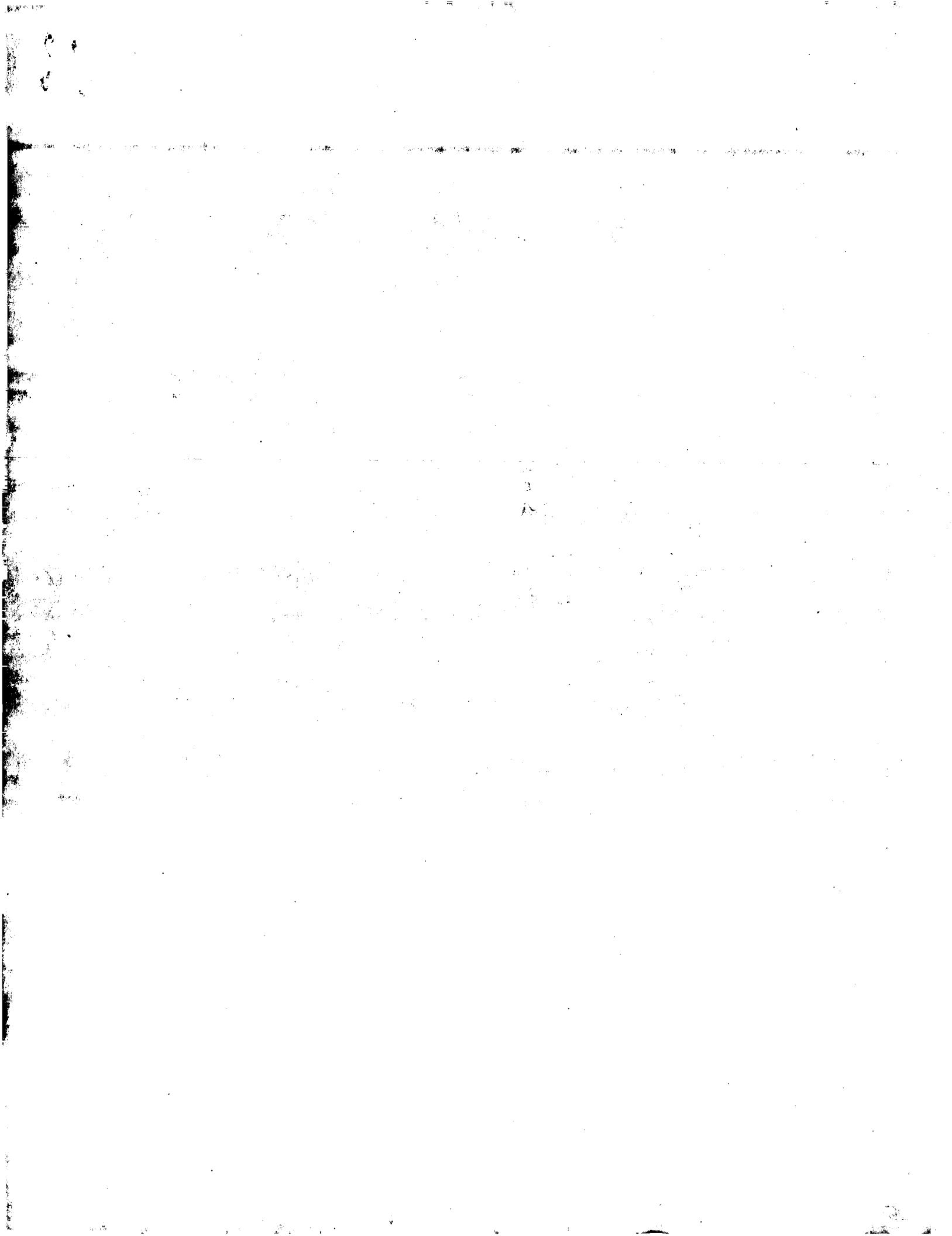
DEPA = residues 403 - 747 of seq ID 2

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; Sequence 2, Application US/10087013
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; APPLICANT: Louis H. Miller
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; APPLICANT: Nobutaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176_001C1
; CURRENT APPLICATION NUMBER: US/10/087,013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013_2
YEEFIIQSISLNDKRRVNNINSEVKKQFVEKLKPTQVATNDTFLNLNLNEGKYCKGLPGEKDITFTNSADD
KGIFYRSIDYCQVCPDCGYKCGKYYTKSDNDRERVNNEYDYPWGVKPTNTIVLXSGNEODITQKLEN
FCNSITNKDKNNQKWECKYKDENINRCKLEONTEINNDNPKISFHNFELAKVYLLRDTIKWNDELT
CINNTTCIDECNRNCICFDRKVKQBEEMWISKKLPTKKKIQQYYSNINNLFGYFFKVMMDKUDKD
EAKWKELEMENIKRKKEEFSNLENNDRYLNELLLDHLKETATICKDNNTNEACETSHNATTP1

```

345
residues



270 280 290 300 310 320
 GYFFKVMKDLDKEAKWKELMENIRKKN---EFSNLE-----NNRDYLENAIE----LLIDHLKETA
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 GMLCALTNGLSESE-KKNILQDYSINKLNNAEKDCGLEFASKPOFLRKYVENSDEFCKRKLEDKVEDV
 170 180 190 200 210 220 230
 TI-CKDNNTNEAC--ETSHNATTNP
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 CTKAKD---TEGCKKNNSNCSVKYCKEKEYENYITGKKTQYESOEG
 240 250 260 270 280

3. US-10-087-013-2 (1-345)

US-10-087-013-9 sequence 9 Application US/10087013

Initial Score = 7 Optimized Score = 46 Significance = -0.58
 Residue Identity = 21% Matches = 52 Mismatches = 178
 Gaps = 46 Conservative Substitutions = 0

70	80	X	90	100	110	120	130	
TNSADDKKGIFTYRSEYCQVCPCGVKGDGTYKTHKSNDRREVNNEDYKPPWGVPNTNIVL-YSGNEOGDI								
PCKMWQKLISSEQIEVNNTIHKCKYTEDAK---WACEN-TKLGEDPGVCMFPR								
X 10 20 30 40								
140	150	160	170	180	190	200		
TOKLENFCNSSTNYKDKNOKWECYKDENINRCKLEQ-NTEINNDNPKI----ISFHNFELWVUTYLIRD								
RONLCVHYLTKLNDSSKEEDLREAIFIKAATETFLRLRQYNSKANVEDDLILHRDMIPPEFRSMFYTFDDYR								
50 60 70 80 90 100 110								
210	220	230						
TIKWNDKLYCINCNTTHCIDECNRNCIDCFDRWYKOK-----EEE-KNSIKLFTKK-KNIQSY								
DI---CLDDI---SEKADHDVTAKKKITAVFOKIGSKTTNGKKVILEREGWKEYGLSINKGMCLASY								
120 130 140 150 160 170 180								
260	270	280	290	300	310	320		
YSNTINNLFECEYFFKVMKDLDKEAKWKELMENIRKKNPF-SNLENNDRYLENAILLDDHLPATICK-								
NTERKKMDEG---VRTYLMKYIK---NNDIKEYLEEPASRPPFLRRAWTEWGEDFVNRKKEBLVSUKKC								
190 210 220 230 240								
330	340	X						
DNNTNEACETSHNATTNP								
DSCCLRNNGTS-NKTCDDMENGCACKTOCERYKKMER								
250 260 X 270 280								

200	210	220	230	240	250	260
AKRPOFLRMILTEWDDYCYTRK--YLKDVOEK-----CKSNDQLRKCDTECNKKGEDVVKY-MKKKWEI						
ASKPQFLRWYVENSDEFCREKKLEDKVEDCILAKADYEGCKNN--KSNNSCVVKCQEYENITGKKTQIE	220	230	240	250	260	270

270	X					
PODKYYKDE-RDKKRF						
SOGKFNFNTERKROKPEVNSYSSKKDASEVLKD	290	X	300			

3. PEPB-PEP (1-276)

US-10-087-013-10 Sequence 10, Application US/10087013

Initial Score = 22	Optimized Score = 106	Significance = -0.49
Residue Identity = 38%	Matches = 121	Mismatches = 147
Gaps = 45	Conservative Substitutions = 0	

X	10	20	30	40	50	60
DCHPKNSNG--YPDMQGNINLVEDPRVCMPROKLCVHFLANDNEIKLQLSQVNLUKEAFIKA						
ETDDIDGCNQKYKAGDKDYGPGWCNSQIHTTINGACHMPROKLCVSLTKTDIRK--ATYIREFIKA						
X	10	20	30	40	50	60
AETTFESWYYSKSKDGGNEGLDELKGSKIPPALFSLMFTFGDYRPLFGNDISKHGEGSKLKEQIDSF	70	80	90	100	110	120
AIETHEAHDRYEEDNG--EAEALKNONIPECFKRQMYTGVDYRQIFFRDIBISTHAYTSGSPKVITIE						
X	80	90	100	110	120	130
KNGDQK---SPNGKTRQEWMPREHSIWEAMLCAL-VKI--GAKKDFDTENYGYNNVKPSDK-STTLEBP	140	150	160	170	180	190
KENDAK'FAKQSNNEELDDWMQHGKDIWEGMLCAUTHKISDEEKKEIKNYSTKLNSSPKGSKVDF	140	150	160	170	180	190
AKRPOFLRWYVENSDEFCREKKLEDKVEDCILAKADYEGCKNN--KSNNSCVVKCQEYENITGKKTQIE	200	210	220	230	240	250
AKRPOFLRWYVENSDEFCREKKLEDKVEDCILAKADYEGCKNN--KSNNSCVVKCQEYENITGKKTQIE	220	230	240	250	260	270
K-----KEWIPQDKYY----KD--ERDKKRF	260	270	X			
KGKFDAAKIDKDEGEYEGESTKQASEYIKK	290	300	310			